REMARKS

The Office Communications of July 3, 2002 and October 21, 2002 have been received and reviewed. The after final amendment submitted October 3, 2002 was not entered as the amendment is alleged to raise new issues that would require further consideration and/or search. The Office is hereby specifically instructed, in accordance with MPEP §706.07(h)(D), that the response of October 3, 2002 is not to be entered.

Rejection of Claims 1-9, 16-18 and 21-25 under 35 U.S.C. § 103 (a) over Saiki *et al.* in view of Bagwell *et al.*:

Claims 1-9, 16-18 and 21-25 stand rejected under 35 U.S.C. § 103 (a) over Saiki *et al.* (U.S. Patent 4,683,194) in view of Bagwell *et al.* (U.S. Patent 5,607,834). Applicants respectfully submit that Saiki *et al.* does not teaches hybridizing at least two probes. The Examiner asserts, for example, bridging pages 3 and 4 of paper 13, that Saiki *et al.* teaches mixing a set of homologous probes.

Saiki *et al.* teaches hybridization of a probe, which regenerates a restriction site present in the probe and complimentary target. The hybridization of the probe to the complimentary target is then detected by cleavage with a restriction enzyme. The method of Saiki *et al.* is a first hybridization of the probe to a sample target sequence to be analyzed and, optionally, to reduce background, a second hybridization of the previously hybridized probe/sample to a second source of target sequence, wherein the second target sequence is composed of an oligonucleotide target having a mismatch in the restriction site. The purpose of the second hybridization is to remove free probe. Thus, the second hybridization requires that the second oligonucleotide be a target sequence and not a probe. Therefore, Saiki teaches the use of only one probe hybridized sequentially to two different sets of target sequences and does not disclose the at least two homologous probes of the present claims.

In addition, the purpose and utility of the Saiki *et al.* invention would be utterly defeated if the oligonucleotide target, having the mismatch, were added simultaneously with the probe.

Furthermore, Saiki does not teach or motivate the use of a non-linear probe, as acknowledged by the Examiner at page 4 of Paper 13.

It is submitted that Saiki does not teach or suggest the use of at least two homologous probes, wherein at least one of the two homologous probes is a non-linear probe. Thus, the cited references do not teach or suggest all of the elements of the claims. Reconsideration and withdrawal of this rejection is respectfully requested.

Rejection of Claims 1-9, 16-18 and 21-25 under 35 U.S.C. § 103 (a) over Saiki *et al.* in view of Guo *et al.*:

Claims 1-9, 16-18 and 21-25 stand rejected under 35 U.S.C. § 103 (a) over Saiki *et al.* (U.S. Patent 4,683,194) in view of Guo *et al.* (Nature Biotechnology, (1997), Vol. 15: 331-335). As previously described, Saiki *et al.* does not teach or suggest at least two probes or non-linear probes. Furthermore, the applicants submit that Guo *et al.* does not teach or suggest a non-linear probe or at least two probes. Figure 1 of Guo *et al.* is cited by the Examiner as disclosing non-linear probes. However, Figure 1 merely illustrates the probe-target hybridization product. The probes of Guo *et al.* include a mismatch and this mismatch is drawn in Figure 1. Mismatches in the probe and/or target, illustrated in Figure 1, are graphically represented as deviations from a straight line. However, a literal view of a straight line is not applicable to the definition of a linear probe.

Gou *et al.* teaches linear probes within the meaning of that term, as understood by a person of ordinary skill in the art. The definition of a non-linear probe was known to a person of ordinary skill in the art at the time the application was filed, as demonstrated by the definition provided in the recognized textbook, BENJAMIN LEWIN, GENES II, 53 (2d. ed. 1985). A non-linear probe is defined as a probe, considered as a single strand, wherein base pairing within the molecule can fix the location of one region relative to another. *Id.*; *see also* the specification at, for example, paragraph 6. Respectfully, the probes of Guo *et al.* are not non-linear probes. For example, the probes disclosed in Figure 2 of Guo *et al.* are based on the following sequence, CAGATCGGCTGAACTCCACA, which is a linear probe. Guo *et al.* does not teach a non-linear probe and does not teach the use of at least two homologous probes, wherein at least one of the two homologous probes is a non-linear probe.

Thus, the cited references do not teach or suggest all of the claim elements.

Reconsideration and withdrawal of this rejection is respectfully requested.

Rejection of Claims 1-9, 16-18 and 21-25 under 35 U.S.C. § 103 (a) over Saiki *et al.* in view of Bagwell *et al.* and further in view of Cronin *et al.*:

Claims 1-9, 16-18 and 21-25 stand rejected under 35 U.S.C. § 103 (a) over Saiki *et al.* (U.S. Patent 4,683,194) in view of Guo *et al.* (Nature Biotechnology, (1997), Vol. 15: 331-335), and further in view of Cronin *et al.* (U.S. Patent No. 6,027,880).

As previously discussed, Guo *et al.* and Saiki *et al.* do not teach all of the claim elements. The Office cites Cronin *et al.* as teaching a method wherein the nucleic acids represent a number of HIV-variants, page 9 of paper 13. Thus, Cronin *et al.* does not supply the missing claim elements. Therefore, the claims are not obvious in light of Guo and Saiki and Cronin. Reconsideration and withdrawal of this rejection is respectfully requested.

Conclusion

In view of the foregoing remarks the application is believed to be in condition for allowance. If questions should remain after consideration of the foregoing, the Examiner is kindly requested to contact applicants' agent at the address or telephone number given herein.

Respectfully submitted,

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Date: January 29, 2003
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Document in ProLaw